

VIA HAND DELIVERY ON JULY 2, 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: He et al.

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Application Serial No.: Unassigned

Art Unit: Unassigned

Filed: Herewith

Examiner: Unassigned

Title: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease-3 and 4

SUBMISSION OF SUBSTITUTE/FORMAL DRAWINGS

Commissioner for Patents
Washington, D.C. 20231

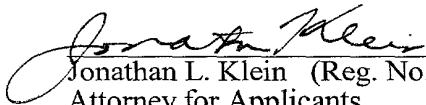
Sir:

Please substitute the attached 7 sheets of formal drawings depicting Figures 1A-B, 2A-B, and 3A-C for the corresponding drawings of Figures 1-3 originally filed with the application. Included herewith, as required under 37 C.F.R. § 1.121(a)(3)(ii), is a copy of the figures as originally filed with changes marked. Acknowledgement of the receipt, approval, and entry of these formal drawings into the above captioned application is respectfully requested.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: JULY 2, 2001


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JLK/LT/ba

1002040-0925660

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FIGURE 1A

1 GCACGAGAACTTTGCTGTGCGCGTTCTCCCGCGCGGGCTCAACTTTGTAGAGCGAGG 60

61 GGCCAACTTGGCAGAGCGCGCGGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT 120

121 GCGGGGACACGGGTGCGCTTTGGGGCTCTTCCACCCCTGCGGAGCGCACTACCCGAGCCAG 180

181 GGGCGGTGCAAGCCCCGCGCGCCCTACCCAGGGCGGCTCCTCCCTCCGCAGCGCCGAGA 240

241 CTTTGTAGTTTCGCTTTTCGCTAAAGGGGCCCCAGACCCTTGCTGCGGAGCGACGGAGAGAG 300

301 ACTGTGCCAGTCCCAGCCGCCCTACCGCCGTGGGAACGATGGCAGATGATCAGGGCTGTA 360
1 M A D D Q G C I 8

361 TTGAAGAGCAGGGGGTTGAGGATTGAGCAAATGAAGATTGAGTGGATGCTAAGCCAGACC 420
9 E E Q G V E D S A N E D S V D A K P D R 28

421 GGTCTCTCGTTTGTACCGTCCCTCTTTCAGTAAGAAGAAGAAAAATGTCACCATGCGATCCA 480
29 S S F V P S L F S K K K K N V T M R S I 48

481 TCAAGACCACCCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAAAGCTGG 540
49 K T T R D R V P T Y Q Y N M N F E K L G 68

541 GCAAATGCATCATAATAAACAACAAGAAGCTTTGATAAAGTGACAGGTATGGGCGTTTCGAA 600
69 K C I I I N N K N F D K V T G M G V R N 88

601 ACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTGTACG 660
89 G T D K D A E A L F K C F R S L G F D V 108

661 TGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAAGCTTCTG 720
109 I V Y N D C S C A K M Q D L L K K A S E 128

721 AAGAGGACCATACAAATGCCGCTGCTTCGCTGCTCCTTAAGCCATGGAGAAGAAA 780
129 E D H T N A A C F A C I L L S H G E E N 148

781 ATGTAATTTATGGGAAAGATGGTGTACACCAATAAAGGATTTGACAGCCCACTTTAGGG 840
149 V I Y G K D G V T P I K D L T A H F R G 168

841 GGGATAGATGCAAAACCCCTTTTAGAGAAACCCAACTCTTCTTCAATCAGGCTTGCCGAG 900
169 D R C K T L L E K P K L F F I Q A C R G 188

901 GGACCGAGCTTGATGATGCCATCCAGGCCGACTCGGGGCCCATCAATGACACAGATGCTA 960
189 T E L D D A I Q A D S G P I N D T D A N 208

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FIGURE 1B

961 ATCCTCGATACAAGATCCCAGTGAAGCTGACTTCCTCTTCGCCTATTCCACGGTTCCAG 1020
209 P R Y K I P V E A D F L F A Y S T V P G 228

1021 GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTGCAAGCCCTCTGCTCCA 1080
229 Y Y S W R S P G R G S W F V Q A L C S I 248

1081 TCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAGATCCTCACCAGGGTGAATGACA 1140
249 L E E H G K D L E I M Q I L T R V N D R 268

1141 GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGAAGCAGA 1200
269 V A R H F E S Q S D D P H F H E K K Q I 288

1201 TCCCTGTGTGGTCTCCATGCTCACCAAGGAAGTCTACTTCAGTCAATAGCCATATCAGG 1260
289 P C V V S M L T K E L Y F S Q 303

1261 GGTACATTCTAGCTGAGAAGCAATGGGTCACTCATTAAATGAATCACATTTTTTTATGCTC 1320

1321 TTGAAATATTAGAAATTTCTCCAGGATTTTAATTTTCAGGAAAATGTATT 1369

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FIGURE 2A

1 GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGCAG 60
61 CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCTTGAAATCCCAG 120
121 GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTTCGGTGGGTGTGCC 180
181 CTGCACCTGCCTCTTCCCGCATTCTCATTAAATAAAGGTATCCATGGAGAACACTGAAAAC 240
1 M E N T E N 6
241 TCAGTGGATTCAAATCCATTAAAAATTGGAACCAAAGATCATACTGGAAGCGAATCA 300
7 S V D S K S I K N L E P K I I H G S E S 26
301 ATGGACTCTGGAATATCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTA 360
27 M D S G I S L D N S Y K M D Y P E M G L 46
361 TGTATAATAATTAATAATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGT 420
47 C I I I N N K N F H K S T G M T S R S G 66
421 ACAGATGTCGATGCAGCAAACCTCAGGGAAACATTCAGAAACTTGAAATATGAAGTCAGG 480
67 T D V D A A N L R E T F R N L K Y E V R 86
481 AATAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAA 540
87 N K N D L T R E E I V E L M R D V S K E 106
541 GATCACAGCAAAGGAGCAGTTTGTGTTGTGCTTCTGAGCCATGGTGAAGAAGGAATA 600
107 D H S K R S S F V C V L L S H G E E G I 126
601 ATTTTTGGAACAAATGGACCTGTTGACCTGAAAAAAATAACAACTTTTTCAGAGGGGAT 660
127 I F G T N G P V D L K K I T N F F R G D 146
661 CGTTGTAGAAGTCTAACTGGAAAACCCAACTTTTCATTATTCAGGCCTGCCGTGGTACA 720
147 R C R S L T G K P K L F I I Q A C R G T 166
721 GAACTGGACTGTGGCATTGAGACAGACAGTGGTGTGATGATGACATGGCGTGTCATAAA 780
167 E L D C G I E T D S G V D D D M A C H K 186
781 ATACCAGTGGAGGCCGACTTCTGTATGCACTCCACAGCACCTGGTTATTATTCTTGG 840
187 I P V E A D F L Y A Y S T A P G Y Y S W 206

095566.0204

[illegible]

841 CGAAATTCAAAGGATGGCTCCTGGTTCATCCAGTCGCTTTGTGCCATGCTGAAACAGTAT 900
207 R N S K D G S W F I Q S L C A M L K Q Y 226

901 GCGGACAAGCTTGAATTTATGCACATTCTTACCCGGGTTAACCGAAAGGTGGCAACAGAA 960
227 A D K L E F M H I L T R V N R K V A T E 246

961 TTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAAAGAAACAGATTCCATGTATTGTT 1020
247 F E S F S F D A T F H A K K Q I P C I V 266

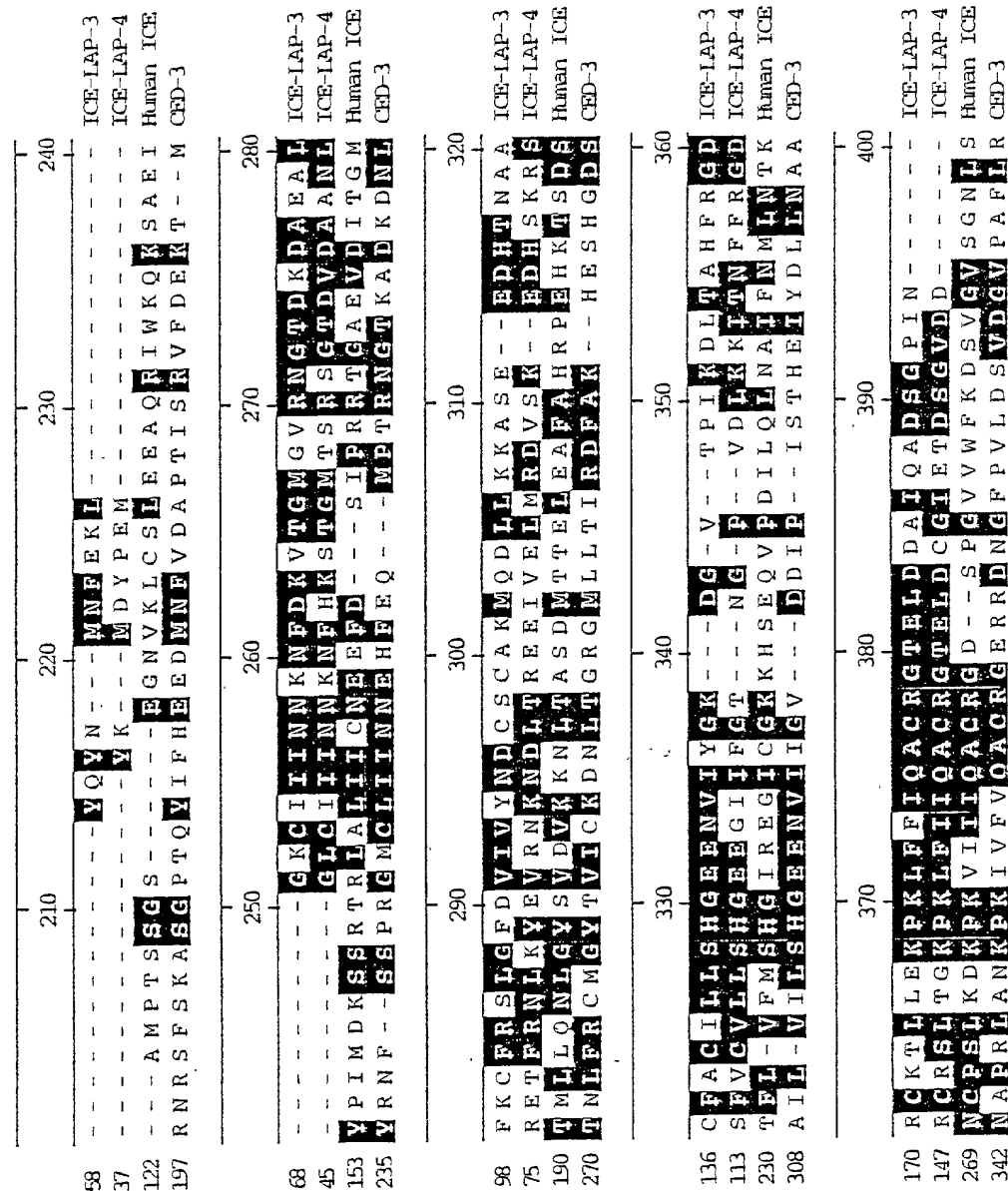
1021 TCCATGCTCACAAAAGAACTCTATTTTATCACTAAAGAAATGGTTGGTTGGTGGTTTTT 1080
267 S M L T K E L Y F Y H * 277

1081 TTTAGTTTGTATGCCAAGTGAGAAGATGGTATATTTGGGTACTGTATTCCCTCTCATTG 1140

1141 GGGACCTACTCTCATGCTG 1159

FIGURE 3A

	10	20	30	40	
1	MAD D	O			ICE-LAP-3
1	MEN T	E			ICE-LAP-4
1	MAD K V L K E K	R K L F I R S M			Human ICE
1	M M R Q	D R R S L L E R N I M M F S S H L K V D E I L E V L I A K Q V L N			CED-3
16	S A N E D S V D A				ICE-LAP-3
16		L E P			ICE-LAP-4
37	K E E M E K V K R E N A T V M D K T R A L I D S V				Human ICE
38	S D N G D M I N S - C G T V R E K R R E I V K A V Q R R G D V A E D A F Y D A L				CED-3
32					ICE-LAP-3
25					ICE-LAP-4
62					Human ICE
77	R S T G H E G L A E V L E P L A R S V D S N A V E F E C P M S P A S H R R S R A				CED-3
49					ICE-LAP-3
37					ICE-LAP-4
78					Human ICE
117	L S P A G V T S P T R V H R D S V S V S S F T S V Q D I Y S R A R S R S R				CED-3
58					ICE-LAP-3
37					ICE-LAP-4
99					Human ICE
157	A L H S S D R H N Y S S P P V N A E P S Q P S S A N S S F T G C S S L G Y S S S				CED-3



ICE-LAP-3
ICE-LAP-4
Human ICE
CED-3

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

1 GCACGAGAACTTTGCTGTGCGCGTTCTCCCGCGCGCGGGCTCAACTTTGTAGAGCGAGG

61 GGCCAACTTGGCAGAGCGCGCGGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT

1 1 M R

121 GCGGGGACACGGGTGCGCTTTGGGCTCTTCCACCCCTGCGGAGCGCACTACCCCGAGCCAG

3 A G T R V A L G S S T P A E R T T P S Q

181 GGGCGGTGCAAGCCCCGCGGCCCTACCCAGGGCGGCTCCTCCCTCCGCAGCGCCGAGA

23 G R C K P R P A L P R A A P P S A A P R

241 CTTTTAGTTTCGCTTTTCGCTAAAGGGGCCCCAGACCTTGCTGCGGAGCGACGGAGAGAG

43 L L V S L S L K G P Q T L A A E R R R E

301 ACTGTGCCAGTCCCAGCCGCCCTACCGCCGTGGGAACGATGGCAGATGATTCAGGGCTGT

63 T V P V P A A L P P W E R W Q M I Q G C

361 ATTGAAGAGCAGGGGGTTGAGGATTGAGCAAATGAAGATTCAGTGGATGCTAAGCCAGAC

83 I E E Q G V E D S A N E D S V D A K P D

421 CGGTCCTCGTTTGTACCGTCCCTCTTCAGTAAGAAGAAGAAAAATGTCACCATGCGATCC

103 R S S F V P S L F S K K K K N V T M R S

481 ATCAAGACCACCCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAGAGCTG

123 I K T T R D R V P T Y Q Y N M N F E K L

541 GGCAAATGCATCATAATAACAACAAGAACTTTGATAAAGTGACAGGTATGGGCGTTTGA

143 G K C I I I N N K N F D K V T G M G V R

601 AACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTGTAC

163 N G T D K D A E A L F K C F R S L G F D

661 GTGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAGCTTCT

183 V I V Y N D C S C A K M Q D L L K K A S

721 GAAGAGGACCATACAAATGCCGCGCTTCGCGCTGCATCCTCTTAAGCCATGGAGAAGAA

203 E E D H T N A A C F A C I L L S H G E E

781 AATGTAATTTATGGGAAGATGGTGTACACCAATAAAGGATTTGACAGCCCCTTTAGG

223 N V I Y G K D G V T P I K D L T A H F R

841 GGGGATAGATGCAAAACCCTTTTAGAGAAACCCAAACTCTTCTTCATTGAGGCTTGCCGA

243 G D R C K T L L E K P K L F F I Q A C R

901 GGGACCGAGCTTGATGATGGCATCCAGGCCGACTCGGGGCCCATCAATGACACAGATGCT

263 G T E L D D G I Q A D S G P I N D T D A

961 AATCCTCGATACAAGATCCCAGTGGAGCTGACTTCCTCTTCGCTATTCCACGGTTCCA

283 N P R Y K I P V E A D F L F A Y S T V P

1021 GGCTATTACTCGTGGAGGAGCCAGGAAGAGGCTCCTGGTTTGTGCAAGCCCTCTGCTCC

303 G Y Y S W R S P G R G S W F V Q A L C S

1081 ATCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAAATCCTCCACCAGGGTGAATGA

323 I L E E H G K D L E I M Q I L H Q G E *

1141 CAGAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGAAGCA

1201 GATCCCCTGTGTGGTCTCCATGCTCACCAAGGAAGCTCTACTTCAGTCAATAGCCATATCA

1261 GGGGTACATTCTAGCTGAGAAGCAATGGGTCACTCATTGAATGACATTTTTTTTATGC

1321 TCTTGAAATATTGAGAAATCTCCAGGATTTTAATTTGAGGAAAATGTATT

Figure 1

1 GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGCAG
61 CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCTTGAAATCCCAG
121 GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTTCGGTGGGTGTGCC
181 CTGCACCTGCCTCTTCCCGCATTCTCATTAAATAAAGGTATCCATGGAGAACACTGAAAAC
1 M E N T E N
241 TCAGTGGATTCAAAATCCATTAAAAATTTGGAACCAAAGATCATACATGGAAGCGAATCA
7 S V D S K S I K N L E P K I I H G S E S
301 ATGGACTCTGGAATATCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTA
27 M D S G I S L D N S Y K M D Y P E M G L
361 TGTATAATAATTAATAATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGT
47 C I I I N N K N F H K S T G M T S R S G
421 ACAGATGTCGATGCAGCAAACCTCAGGGAAACATTTCAGAACTTGAAATATGAAGTCAGG
67 T D V D A A N L R E T F R N L K Y E V R
481 AATAAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAA
87 N K N D L T R E E I V E L M R D V S K E
541 GATCACAGCAAAGGAGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATA
107 D H S K R S S F V C V L L S H G E E G I
601 ATTTTTGGAACAAATGGACCTGTTGACCTGAAAAAATAACAACTTTTTTCAGAGGGGAT
127 I F G T N G P V D L K K I T N F F R G D
661 CGTTGTAGAAGTCTAACTGGAAAACCCAACTTTTCATTATTTCAGGCCTGCCGTGGTACA
147 R C R S L T G K P K L F I I Q A C R G T
721 GAACTGGACTGTGGCATTGAGACAGACAGTGGTGTGATGATGACATGGCGTGTCATAAA
167 E L D C G I E T D S G V D D D M A C H K
781 ATACCAGTGGAGGCCGACTTCTGTATGCATACTCCACAGCACCTGGTTATTATTCTTGG
187 I P V E A D F L Y A Y S T A P G Y Y S W
841 CGAAATTCAAAGGATGGCTCCTGGTTCATCCAGTCGCTTTGTGCCATGCTGAAACAGTAT
207 R N S K D G S W F I Q S L C A M L K Q Y
901 GCCGACAAGCTTGAATTTATGCACATTCTTACCCGGGTTAACCGAAAGGTGGCAACAGAA
227 A D K L E F M H I L T R V N R K V A T E
961 TTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAAAGAAACAGATTCCATGTATTGTT
247 F E S F S F D A T F H A K K Q I P C I V
1021 TCCATGCTCACAAAAGAACTCTATTTTTATCACTAAAGAAATGGTTGGTTGGTGGTTTTT
267 S M L T K E L Y F Y H *
1081 TTTAGTTTGTATGCCAAGTGAGAAGATGGTATATTTGGGTACTGTATTTCCCTCTCATTG
1141 GGGACCTACTCTCATGCTG

Figure 2

